

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: O'BRIEN, JOHN S.
KISHIMOTO, YASUO
- (ii) TITLE OF INVENTION: IDENTIFICATION OF PROSAPOSIN AS A
NEUROTROPHIC FACTOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
(B) STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
(C) CITY: NEWPORT BEACH
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92660
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
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(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Israelsen, Ned A.
(B) REGISTRATION NUMBER: 29,655
(C) REFERENCE/DOCKET NUMBER: OBRIEN.002A
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 619-235-8550
(B) TELEFAX: 619-235-0176

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: 22-MER FRAGMENT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
1 5 10 15

Thr Glu Lys Glu Ile Leu
20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 523 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: PROSAPOSIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
1 5 10 15

Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
20 25 30

Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
35 40 45

Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
50 55 60

Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
65 70 75 80

Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
 85 90 95
 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
 100 105 110
 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
 115 120 125
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
 130 135 140
 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
 145 150 155 160
 Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
 165 170 175
 Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
 180 185 190
 Asp Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile Gln
 195 200 205
 Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu His
 210 215 220
 Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile Cys
 225 230 235 240
 Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met Met
 245 250 255
 His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp Glu
 260 265 270
 Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala Ser
 275 280 285
 Lys Asn Val Ile Pro Ala Leu Asp Leu Val Asp Pro Ile Lys Lys His
 290 295 300
 Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu
 305 310 315 320
 Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
 325 330 335
 Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu
 340 345 350
 Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu
 355 360 365

Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu
 370 375 380
 His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val Thr
 385 390 395 400
 Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val Gly
 405 410 415
 Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile Leu
 420 425 430
 Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys
 435 440 445
 Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu Ile
 450 455 460
 Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly Ala
 465 470 475 480
 Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile Trp
 485 490 495
 Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys Asn
 500 505 510
 Ala Val Glu His Cys Lys Arg His Val Trp Asn
 515 520

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: SAPOSIN C
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr
 1 5 10 15

Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe
 20 25 30
 Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln
 35 40 45
 Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu
 50 55 60
 Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PROSAPOSIN cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTACGCCC TCTTCCTCCT GGCCAGCCTC CTGGGCGCGG CTCTAGCCGG CCCGGTCCTT	60
GGACTGAAAG AATGCACCAG GGGCTCGGCA GTGTGGTGCC AGAATGTGAA GACGGCGTCC	120
GACTGCGGGG CAGTGAAGCA CTGCCTGCAG ACCGTTTGGA ACAAGCCAAC AGTGAAATCC	180
CTTCCCTGCG ACATATGCAA AGACGTTGTC ACCGCAGCTG GTGATATGCT GAAGGACAAT	240
GCCACTGAGG AGGAGATCCT TGTTTACTTG GAGAAGACCT GTGACTGGCT TCCGAAACCG	300
AACATGTCTG CTTCATGCAA GGAGATAGTG GACTCCTACC TCCCTGTCAT CCTGGACATC	360
ATTAAAGGAG AAATGAGCCG TCCTGGGGAG GTGTGCTCTG CTCTCAACCT CTGCGAGTCT	420
CTCCAGAAGC ACCTAGCAGA GCTGAATCAC CAGAAGCAGC TGGAGTCCAA TAAGATCCCA	480
GAGCTGGACA TGA CTGAGGT GGTGGCCCCC TTCATGGCCA ACATCCCTCT CCTCCTCTAC	540
CCTCAGGACG GCCCCCGCAG CAAGCCCCAG CCAAAGGATA ATGGGGACGT TTGCCAGGAC	600

TGCATTCAGA TGGTGA CTGA CATCCAGACT GCTGTACGGA CCAACTCCAC CTTTGTCCAG 660
 GCCTTGGTGG AACATGTCAA GGAGGAGTGT GACCGCCTGG GCCCTGGCAT GGCCGACATA 720
 TGCAAGAACT ATATCAGCCA GTATTCTGAA ATTGCTATCC AGATGATGAT GCACATGCAA 780
 CCCAAGGAGA TCTGTGCGCT GGTGTTGGTTC TGTGATGAGG TGAAAGAGAT GCCCATGCAG 840
 ACTCTGGTCC CCGCCAAAGT GGCCTCCAAG AATGTGATCC CTGCCCTGGA ACTGGTGGAG 900
 CCCATTAAGA AGCACGAGGT CCCAGCAAAG TCTGATGTTT ACTGTGAGGT GTGTGAATTC 960
 CTGGTGAAGG AGGTGACCAA GCTGATTGAC AACACAAGA CTGAGAAAGA AATACTCGAC 1020
 GCTTTTGACA AAATGTGCTC GAAGCTGCCG AAGTCCCTGT CGGAAGAGTG CCAGGAGGTG 1080
 GTGGACACGT ACGGCAGCTC CATCCTGTCC ATCCTGCTGG AGGAGGTCAG CCCTGAGCTG 1140
 GTGTGCAGCA TGCTGCACCT CTGCTCTGGC ACGCGGCTGC CTGCACTGAC CGTTCACGTG 1200
 ACTCAGCCAA AGGACGGTGG CTTCTGCGAA GTGTGCAAGA AGCTGGTGGG TTATTTGGAT 1260
 CGCAACCTGG AGAAAAACAG CACCAAGCAG GAGATCCTGG CTGCTCTTGA GAAAGGCTGC 1320
 AGCTTCCTGC CAGACCCTTA CCAGAAGCAG TGTGATCAGT TTGTGGCAGA GTACGAGCCC 1380
 GTGCTGATCG AGATCCTGGT GGAGGTGATG GATCCTTCCT TCGTGTGCTT GAAAATTGGA 1440
 GCCTGCCCCCT CGGCCCATAA GCCCTTGTTG GGAAGTGAAG AGTGTATATG GGGCCCAAGC 1500
 TACTGGTGCC AGAACACAGA GACAGCAGCC CAGTGCAATG CTGTGAGCA TTGCAAACGC 1560
 CATGTGTGGA ACTAGGAGGA GGAATATTCC ATCTTGGCAG AAAGCACAGC ATTGGTTTTT 1620
 TTCTACTTGT GTGTCTGGGG GAATGAACGC ACAGATCTGT TTGACTTTGT TATAAAAATA 1680
 GGGCTCCCCC ACCTCCCCCA TTTCTGTGTC CTTTATTGTA GCATTGCTGT CTGCAAGGGA 1740
 GCCCCTAGCC CCTGGCAGAC ATAGCTGCTT CAGTGCCCCT TTTCTCTCTG CTAGATGGAT 1800
 GTTGATGCAC TGGAGGTCTT TTAGCCTGCC CTTGCATGGC GCCTGCTGGA GGAGGAGAGA 1860
 GCTCTGCTGG CATGAGCCAC AGTTTCTTGA CTGGAGGCCA TCAACCCTCT TGGTTGAGGC 1920
 CTTGTTCTGA GCCCTGACAT GTGCTTGGGC ACTGGTGGGC CTGGGCTTCT GAGGTGGCCT 1980
 CCTGCCCTGA TCAGGGACCC TCCCCGCTTT CCTGGGCCTC TCAGTTGAAC AAAGCAGCAA 2040
 AACAAAGGCA GTTTTATATG AAAGATTAGA AGCCTGGAAT AATCAGGCTT TTTAAATGAT 2100
 GTAATTCCCA CTGTAATAGC ATAGGGATTT TGGAAGCAGC TGCTGGTGGC TTGGGACATC 2160
 AGTGGGGCCA AGGGTTCTCT GTCCCTGGTT CAACTGTGAT TTGGCTTTCC CGTGTCTTTC 2220

CTGGTGATGC CTTGTTTGGG GTTCTGTGGG TTTGGGTGGG AAGAGGGCAA TCTGCCTGAA 2280
 TGTAACCTGC TAGCTCTCCG AAGGCCCTGC GGGCCTGGCT TGTGTGAGCG TGTGGACAGT 2340
 GGTGGCCGCG CTGTGCCTGC TCGTGTGGCC TACATGTCCC TGGCTGTTGA GGCCTGCTT 2400
 CAGCCTGCAC CCCTCCCTTG TCTCATAGAT GCTCCTTTTG ACCTTTTCAA ATAAATATGG 2460
 ATGGCGAGCT CCTAGGCCTC TGGCTTCCTG GTAGAGGGCG GCATGCCGAA GGGTCTGCTG 2520
 GGTGTGGATT GGATGCTGGG GTGTGGGGGT TGAAGCTGT CTGTGGCCCA CTTGGGCACC 2580
 CACGCTTCTG TCCAATTCTG GTTGCCAGGA GACAGCAAGC AAAGCCAGCA GGACATGAAG 2640
 TTGCTATTAA ATGGAATTCTG TGATTTTGT TTTGCACTAA AGTTTCTGTG ATTTAACAAT 2700
 AAAATTCTGT TAGCCAGAAA AAAAAAAAAA AAAAAAAAAA 2740

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: 18-MER FRAGMENT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Tyr Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
 1 5 10 15

Ile Leu